

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 11:15:29 ; Search time 9316.36 Seconds
(without alignments)
65.601 Million cell updates/sec

Title: US-10-086-184-2

Perfect score: 21

Sequence: 1 gtcgctcgtatagagctgacc 21

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenEmbl:

- 1: gb_ba:*
- 2: gb_hcg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_pro:*
- 11: gb_scs:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
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- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_scs:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_hcg_hum:*
- 31: em_hcg_inv:*
- 32: em_hcg_other:*
- 33: em_hcg_mus:*
- 34: em_hcg_pin:*
- 35: em_hcg_rtd:*
- 36: em_hcg_mam:*
- 37: em_hcg_vrt:*
- 38: em_sy:*
- 39: em_hcg_hum:*
- 40: em_hcg_mus:*
- 41: em_hcg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.6	64.8	25	6	AX328796 Sequence
C 2	13.4	63.8	21	6	AX019207 Sequence
C 3	12.8	61.0	39	6	AX418584 Sequence
C 4	12.6	60.0	27	6	AR084832 Sequence
C 5	12.4	59.0	17	6	A20005 SEQ ID NO: 1
C 6	12.4	59.0	17	6	A20013 SEQ ID NO: 1
C 7	12.4	59.0	17	6	A20029 SEQ ID NO: 1
C 8	12.4	59.0	17	6	113201 Sequence 23
C 9	12.4	59.0	17	6	113217 Sequence 45
C 10	12.4	59.0	20	6	AX417158 Sequence
C 11	12.4	59.0	23	6	AX417148 Sequence
C 12	12.4	59.0	31	6	AX417152 Sequence
C 13	12.4	59.0	32	6	AR175460 Sequence
C 14	12.4	59.0	36	6	AX417156 Sequence
C 15	12.2	58.1	24	6	AX443895 Sequence
C 16	12.2	58.1	25	6	AX447871 Sequence
C 17	12.2	58.1	26	6	AX038056 Sequence
C 18	12.2	58.1	26	6	AX038057 Sequence
C 19	12.2	58.1	26	6	AX327686 Sequence
C 20	12.2	58.1	27	6	E36449 DNA polymerase 113350 Sequence 7
C 21	12.2	58.1	27	6	113350 Sequence 7
C 22	12.2	58.1	32	6	118872 Sequence 18
C 23	12.2	58.1	32	6	136798 Sequence 18
C 24	12.2	58.1	32	6	156002 Sequence 18
C 25	12.2	58.1	33	6	E36466 DNA polymerase 113350 Sequence 18
C 26	12.2	58.1	35	6	AX120003 Sequence
C 27	12.2	58.1	40	6	AX107556 Sequence
C 28	12.2	57.1	22	6	A22025 Sequence
C 29	12.2	57.1	24	6	AR093406 Sequence
C 30	12.2	57.1	24	6	AR172153 Sequence
C 31	12.2	57.1	24	6	BD000251 Oligonucleotide BD000359 Method for BD000795 Oligonucleotide E30931 Amplification
C 32	12.2	57.1	24	6	BD000795 Oligonucleotide E30931 Amplification
C 33	12.2	57.1	24	6	E30931 Amplification
C 34	12.2	57.1	24	6	E30931 Amplification
C 35	12.2	57.1	25	6	AX197037 Sequence
C 36	12.2	57.1	33	6	186650 Sequence 29
C 37	12.2	57.1	37	6	AR181187 Sequence
C 38	11.8	56.2	20	6	AR016119 Sequence
C 39	11.8	56.2	20	6	AR019117 Sequence
C 40	11.8	56.2	20	6	AX293144 Sequence
C 41	11.8	56.2	20	6	E07026 Primer, 9/1
C 42	11.8	56.2	22	6	AR108179 Sequence
C 43	11.8	56.2	22	6	AR148629 Sequence
C 44	11.8	56.2	22	6	AR206680 Sequence
C 45	11.8	56.2	22	6	AX085790 Sequence

ALIGNMENTS

RESULT 1	AX328796	25 bp	DNA	linear	PAT 08-JAN-2002
LOCUS	AX328796				
DEFINITION	Sequence 293 from Patent EP1164203.				
ACCESSION	AX328796				
VERSION	AX328796.1				
KEYWORDS	GI:18101995				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1				
AUTHORS	Koester, H., Little, D.P., Braun, A., Jurinke, C., van den Boom, D., Xiang, G., Lough, D.M., Ruppert, A. and Hillekamp, F.				
TITLE	Dna diagnostics based on mass spectrometry				
JOURNAL	Patent: EP 1164203-A 293 19-DEC-2001;				

SEQUENOM, INC. (US)

FEATURES Location/Qualifiers
source 1..25
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 8 a 6 c 4 g 7 t

Query Match 64.8%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCTACTGATAGCTGTAC 20
DB 20 GTTCTACTGATAGAAATTAC 1

RESULT 2
LOCUS AX019207/c 21 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 45 from Patent WO9941393.

ACCESSION AX019207
VERSION AX019207.1 GI:10043239

KEYWORDS

SOURCE synthetic construct.

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 21)

Acland, D.P., Blake, A.N., Lee, M.D., Osborn, R.W., Robinson, M.P. and

Windsor, J.D.

INSECTICIDAL PEPTIDES

Patent: WO 9941393-A 45 19-AUG-1999;

ACLAND DAVID PAUL (GB); BLAKE ANDREW NICHOLAS (GB); LEE MICHAEL

DAVID (GB); OSBORN RUPERT WILLIAM (GB); ZENECA LTD (GB); ROBINSON

MICHAEL PETER (GB); WINDASS JOHN DAVID (GB)

Location/Qualifiers

1..21

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="primer"

BASE COUNT 5 a 5 c 5 g 6 t

Query Match 63.8%; Score 13.4; DB 6; Length 21;

Best Local Similarity 93.3%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCTACTGATAGAG 15
DB 18 GCCTACTGATAGAG 4

RESULT 3

LOCUS AX418584 39 bp DNA linear PAT 18-JUN-2002

DEFINITION Sequence 70 from Patent WO0200006.

ACCESSION AX418584

VERSION AX418584.1 GI:21523449

KEYWORDS

SOURCE synthetic construct.

ORGANISM artificial sequences.

REFERENCE 1

Lu, Y. and Li, J.

Nucleic acid enzyme biosensor for ions

Patent: WO 0200006-A 70 03-JUN-2002;

THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)

Location/Qualifiers

1..39

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="Zn-DNA"

BASE COUNT 10 a 5 c 9 g 15 t

ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 39;
Best Local Similarity 87.5%; Pred. No. 4.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCTACTGATAGAGTGT 18
DB 9 GCTACTGAAATAGTGT 24

RESULT 4

LOCUS AR084832/c 27 bp DNA linear PAT 01-SEP-2000

DEFINITION Sequence 16 from patent US 5981225.

ACCESSION AR084832

VERSION AR084832.1 GI:10011603

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 27)

Kochanek, S. and Schledner, G.

Gene transfer vector, recombinant adenovirus particles containing

the same, method for producing the same and method of use of the

same

Patent: US 5981225-A 16 09-NOV-1999;

Location/Qualifiers

1..27

/organism="unknown"

BASE COUNT 11 a 5 c 5 g 6 t

Query Match 60.0%; Score 12.6; DB 6; Length 27;

Best Local Similarity 78.9%; Pred. No. 6.1e+04;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCTACTGATAGCTGTA 19
DB 24 GTGTTACTCTATAGCTCTA 6

RESULT 5

LOCUS A20005/c 17 bp DNA linear PAT 14-JUL-1995

DEFINITION SEQ ID NO: 13; Oligonucleotide BB3510.

ACCESSION A20005

VERSION A20005.1 GI:1247838

KEYWORDS

SOURCE synthetic construct.

ORGANISM artificial sequences.

Location/Qualifiers

1..17

/organism="synthetic construct"

/db_xref="taxon:32630"

BASE COUNT 7 a 4 c 2 g 4 t

ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 17;

Best Local Similarity 92.9%; Pred. No. 8.1e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTACTGATAGAG 15
DB 14 TGCTACTGATAGTG 1

RESULT 6

LOCUS A20013/c 17 bp DNA linear PAT 14-JUL-1995

DEFINITION SEQ ID NO: 21; Oligonucleotide BB3510.

ACCESSION A20013

VERSION	A20013.1	GI:1247846
KEYWORDS	.	
SOURCE	. synthetic construct.	
ORGANISM	. synthetic construct	
FEATURES	artificial sequences. location/Qualifiers 1..17 /organism="synthetic construct" /db_xref="taxon:32630"	
BASE COUNT	7 a 4 c 2 g 4 t	
ORIGIN		
Query Match	59.0%; Score 12.4; DB 6;	Length 17;
Best Local Similarity	92.9%; Pred. No. 8.1e+04;	
Matches 13; Conservative	0; Mismatches 1;	Indels 0; Gaps 0;
Oy	2 TGCTACTGATAGAG 15 Db 14 TGCTACTGATAGTG 1	
RESULT 8		
LOCUS	I113201	17 bp DNA linear PAT 26-JUL-1995
DEFINITION	Sequence 23 from patent US 5434073.	
ACCESSION	I113201	
VERSION	I113201.1 GI:910549	
KEYWORDS	.	
SOURCE	. Unknown.	
ORGANISM	. Unknown.	
REFERENCE	Unclassified. 1 (bases 1 to 17) Dawson,K., Hunter,M.G. and Czaplowski,L.G. Fibronolytic and anti-chromoblastic cleavable dimers Patent: US 5434073-A 23 18-JUN-1995; JOURNAL location/Qualifiers PATENT 1..17 source /organism="unknown"	
BASE COUNT	7 a 4 c 2 g 4 t	
ORIGIN		
Query Match	59.0%; Score 12.4; DB 6;	Length 17;
Best Local Similarity	92.9%; Pred. No. 8.1e+04;	
Matches 13; Conservative	0; Mismatches 1;	Indels 0; Gaps 0;
Oy	2 TGCTACTGATAGAG 15 Db 14 TGCTACTGATAGTG 1	
FEATURES	Location/Qualifiers 1..17 /organism="synthetic construct" /db_xref="taxon:32630"	
BASE COUNT	7 a 4 c 2 g 4 t	
ORIGIN		
Query Match	59.0%; Score 12.4; DB 6;	Length 17;
Best Local Similarity	92.9%; Pred. No. 8.1e+04;	
Matches 13; Conservative	0; Mismatches 1;	Indels 0; Gaps 0;
Oy	2 TGCTACTGATAGAG 15 Db 14 TGCTACTGATAGTG 1	
BASE COUNT	7 a 4 c 2 g 4 t	
ORIGIN		
Query Match	59.0%; Score 12.4; DB 6;	Length 17;
Best Local Similarity	92.9%; Pred. No. 8.1e+04;	
Matches 13; Conservative	0; Mismatches 1;	Indels 0; Gaps 0;
Oy	2 TGCTACTGATAGAG 15 Db 14 TGCTACTGATAGTG 1	
BASE COUNT	7 a 4 c 2 g 4 t	
ORIGIN		

[illegible]

REFERENCE 1
 AUTHORS Golovko, A. and Hall, G.J.
 TITLE Modified tet -inducible system for regulation of gene expression in plants
 JOURNAL Patent: WO 0220811-A 25 14-MAR-2002;
 BASF Plant Science GmbH (DE)
 FEATURES
 source 1. .23
 /db_xref="taxon:32630"
 /db_xref="taxon:32630"
 BASE COUNT 7 a 5 c 5 g 6 t
 ORIGIN
 Query Match 59.0%; Score 12.4; DB 6; Length 23;
 Best Local Similarity 92.9%; Pred. No. 8e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ACTGATAGAGTGA 19
 |||||
 Db 10 ACTGATAGAGTGA 23

RESULT 12
 LOCUS AX417152 31 bp DNA linear PAT 14-JUN-2002
 DEFINITION Sequence 29 from Patent WO0220811.
 ACCESSION AX417152
 VERSION AX417152.1 GI:21449739
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Golovko, A. and Hall, G.J.
 TITLE Modified tet -inducible system for regulation of gene expression in plants
 JOURNAL Patent: WO 0220811-A 29 14-MAR-2002;
 BASF Plant Science GmbH (DE)
 FEATURES
 source 1. .31
 /db_xref="taxon:32630"
 /db_xref="taxon:32630"
 BASE COUNT 12 a 5 c 5 g 9 t
 ORIGIN
 Query Match 59.0%; Score 12.4; DB 6; Length 31;
 Best Local Similarity 92.9%; Pred. No. 7.9e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ACTGATAGAGTGA 19
 |||||
 Db 18 ACTGATAGAGTGA 31

RESULT 13
 LOCUS ARI75460 32 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 2 from patent US 6309829.
 ACCESSION ARI75460
 VERSION ARI75460.1 GI:17916759
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1
 AUTHORS Livak, K.J., Lowe, A.L. and Blasband, A.J.
 TITLE length determination of nucleic acid repeat sequences by discontinuous primer extension
 JOURNAL Patent: US 6309829-A 2 30-OCT-2001;
 FEATURES
 source 1. .32
 /db_xref="taxon:32630"
 /db_xref="taxon:32630"

BASE COUNT 12 a 2 c 9 g 9 t
 ORIGIN
 Query Match 59.0%; Score 12.4; DB 6; Length 32;
 Best Local Similarity 92.9%; Pred. No. 7.9e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ACTGATAGAGTGA 19
 |||||
 Db 7 ACTGATAGAGTGA 20

RESULT 14
 LOCUS AX417156 36 bp DNA linear PAT 14-JUN-2002
 DEFINITION Sequence 33 from Patent WO0220811.
 ACCESSION AX417156
 VERSION AX417156.1 GI:21449743
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Golovko, A. and Hall, G.J.
 TITLE Modified tet -inducible system for regulation of gene expression in plants
 JOURNAL Patent: WO 0220811-A 33 14-MAR-2002;
 BASF Plant Science GmbH (DE)
 FEATURES
 source 1. .36
 /db_xref="taxon:32630"
 /db_xref="taxon:32630"

BASE COUNT 10 a 7 c 5 g 14 t
 ORIGIN
 Query Match 59.0%; Score 12.4; DB 6; Length 36;
 Best Local Similarity 92.9%; Pred. No. 7.8e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ACTGATAGAGTGA 19
 |||||
 Db 23 ACTGATAGAGTGA 36

RESULT 15
 LOCUS AX443895 24 bp DNA linear PAT 03-JUL-2002
 DEFINITION Sequence 350 from Patent WO0216649.
 ACCESSION AX443895
 VERSION AX443895.1 GI:21691173
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Gunderson, K.
 TITLE Probes and decoder oligonucleotides
 JOURNAL Patent: WO 0216649-A 350 28-FEB-2002;
 Illumina, Inc. (US)
 FEATURES
 source 1. .24
 /db_xref="taxon:32630"
 /db_xref="taxon:32630"
 /note="Computer Generated Probe Sequence."

BASE COUNT 4 a 9 c 5 g 6 t
 ORIGIN
 Query Match 58.1%; Score 12.2; DB 6; Length 24;
 Best Local Similarity 82.4%; Pred. No. 1e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCTACTGATAGAGTGA 19
 |||||

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Db 18 GCACTGTAGAGCGTA 2

Search completed: March 26, 2003, 16:47:40
Job time : 9318.36 secs

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